

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 05:34:19 ; Search time 9440 Seconds  
 (without alignments)  
 11588.752 Million cell updates/sec

Title: US-09-989-734-A-351

Perfect score: 2524

Sequence: 1 cgccaagcatgcagtaaagg.....ataaagcctttgcaagataa 2524

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

- 1: gb\_ba:\*
- 2: gb\_htg:\*
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- 6: gb\_pat:\*
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## SUMMARIES

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4	2476.6	98.1	2508	6	BD248889	BD248889 47 human
5	2412.4	95.6	2527	6	BD248857	BD248857 47 human
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9	1862.6	73.8	245880	2	AC079387	AC079387 Homo sapi
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c 37	72.2	2.9	172530	2	AC116740	AC116740 Mus muscu
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c 40	71.4	2.8	208166	2	AC131980	AC131980 Mus muscu
c 41	71.4	2.8	313650	2	AC131995	AC131995 Mus muscu
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## ALIGNMENTS

## RESULT 1

AX697283

LOCUS AX697283 2524 bp DNA linear PAT 02-APR-2003

DEFINITION Sequence 351 from Patent WO0078961.

ACCESSION AX697283

VERSION AX697283.1 GI:29498434

## KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE 1

AUTHORS Ferrara,N., Stewart,T.A., Willianis,P.M., Baker,K.P., Desnoyers,L.,  
Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,  
Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,  
Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the sameJOURNAL Patent: WO 0078961-A 351 28-DEC-2000;  
Genentech Inc. (US)

## FEATURES Location/Qualifiers

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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 241  
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Qy 961  
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## RESULT 2

AY358534

LOCUS AY358534 2524 bp mRNA linear PRI 03-OCT-2003

DEFINITION Homo sapiens clone DNA76396 ESRM828 (UNQ828) mRNA, complete cds.

ACCESSION AY358534

VERSION AY358534.1 GI:37182190

KEYWORDS FLI\_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2524)



AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,  
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,  
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,  
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,  
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
Goddard,A., Wood,W.I. and Godowski,P.

TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment

JOURNAL Genome Res. 13 (10), 2265-2270 (2003)

PUBMED 12975309

REFERENCE 2 (bases 1 to 2524)

AUTHORS Clark,H.F.

TITLE Direct Submission

JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES: Location/Qualifiers

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Qy 1861  
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Qy 2521 ATAA 2524  
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### RESULT 3

AK091656

LOCUS AK091656 2538 bp mRNA linear PRI 15-JUL-2003

DEFINITION Homo sapiens cDNA FLJ34337 fis, clone FEBRA2009437.

ACCESSION AK091656

VERSION AK091656.1 GI:21750076

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

### REFERENCE 1

AUTHORS Tanigami,A., Fujiwara,T., Shibahara,T., Goto,Y., Hirao,M.,  
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Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,  
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Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K.,  
Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,  
Sugano,S., Nagahari,K., Masuko,Y., Nagai,K. and Isogai,T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

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AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

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COMMENT NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
Research Association for Biotechnology (RAB); cDNA library  
construction: Helix Research Institute (HRI) (supported by Japan  
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,  
HRI, and Biotechnology Center, National Institute of Technology and  
Evaluation; clone selection for full insert sequencing: HRI and  
RAB; annotation: HRI and RAB.

FEATURES Location/Qualifiers

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/dev\_stage="fetal"  
/note="cloning vector: pME18SFL3"

ORIGIN

Query Match 99.7%; Score 2517.2; DB 9; Length 2538;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2519; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 61  
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Db 317  
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